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                                         106:BCT 107:GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV 112:MAM 113:VRT 114:PHG 115:PLN 116:PRI1 117:PRI2 118:ROD 119:SYN 120:UNA 121:VRL u-emb1:0_99 122:part1
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Gap 6
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Listing first 45 summaries

    n.a. database search, using Smith-Waterman algorithm

  Mean 11.533;
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1:BCT 2:EUN 3:GENI 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV
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ALIGNMENTS

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			alifiers	Location/Qualifiers	ŗ	FEATURES
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			80	ngal disea:	control fungal disease	
thei	Plant inhibitors of fungal polygalacturonases and their use to	ygalactur	fungal pol	bitors of :	Plant inhil	TITLE
•	Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.	well,A. a	h, J.M., Ро	, Labavitel	Bennett, A.	AUTHORS
				(bases 1 to 215)	1 (bases	REFERENCE
				ed.	Unclassified.	
					Unknown.	ORGANISM
					Unknown.	SOURCE
					•	KEYWORDS
					g1819054	NID
					128278	ACCESSION
		830.	nt US 5569	from pate	Sequence 5 from patent US 5569830	DEFINITION
30-OCT-1996	PAT		DNA	215 bp	128278	LOCUS
						RESULT 1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Bennett,A., Labavitth,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use
control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
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                    Eukaryotae; mitochondrial eukaryotes; Alveolata; hypotrichs; Stichotrichida; Oxytricha. 1 (bases 1 to 354)
Doak, T.G., Doerder, F.P., Jahn, C.L. and Herrick, G.
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Pred. No. 1.31e-04;
80; Mismatches 86
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Oncological Science, University of Utah, School of Med. Rm5C334, USA, UT 84132, USA
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Direct Submission
Submitted (11-FEB-1997) Oncological Science,
School of Med. Rm55334, USA, UT 84132, USA
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Mismatches 2
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Matches
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00189259 standard; DN
089259;
91881675
13-MAR-1997 (Rel. 51, C
13-MAR-1997 (Rel. 51, I
0xytricha fallax 57kD z
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Doak T.G., Doerder F.P., Jahn C.L., Herrick G.;

Doak T.G., Doerder F.P., Jahn C.L., Herrick G.;

"A proposed superfamily of transposase genes: transposon-like elements in ciliated protozoa and a common 'D35E' motif";

Proc. Natl. Acad. Sci. U.S.A. 91:942-946(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxytricha fallax
Eukaryotae; mitochondrial eukaryotes; Alv
hypotrichs; Stichotrichida; Oxytrichidae;
                                                                                                                                                                                Sg
                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (11-FEB-1997)
Oncological Science, Uni
USA, UT 84132, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Witherspoon D.J., Doak T.G., Williams K., Seger J., Herrick G. "Selection on the protein-coding genes of the TBE1 family of transposable elements in the ciliates Oxytricha fallax and O. trifallax";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished.
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larity 23.7%;
Conservative
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QAXEXXXVXXXRNXLXSEXTKIMIKIQYKKIPVLAQIDLDTSLQSYLILEDSFDKKVI
XDHQYAYKVYPFNYL"
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/product="57kD zinc finger/protein chimera"
/db_xref="pID:g1881676"
/transl_table=6
                                                                                                                                                                                                      /note-"this is a bulk sequence that was gene
PCR product that represents many transposon
AXEXXXVXXXRNXLXSEXTKIMIKIQYKKIPVLAQIDLDTSLQSYLILEDSFDKKVIX
                                             /product="57kD zinc finger/protein chimera"
/transl_table=6
/db_xref="PID:91881676"
/translation="HTRDLXKHLLKAHKKXXEXEXXXXXLKXLXKKKAREXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                        /transposon="TBE1"
                                                                                                                                                                                                                                                                                   /organism="Oxytricha
/strain="9D1"
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of Utah, School o
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Mismatches 36;
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Carassius
L23876
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eutebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Cyprininae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1441)
Cohen, I., Shani, Y. and Schwartz, M.
Cloning and characteristics of fish glial fibrillary acidic protein: implications for optic nerve regeneration
J. Comp. Neurol. 334 (3), 431-443 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   966477 1441 bp mRNA
glial fibrillary acidic protein {clone
brain, mRNA Partial, 1441 nt].
866477
   Carassius
                                g388622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 139059] from the original journal article. This sequence comes from Fig. 1.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                   /product-"glial fibrillary acidic protein"
/db_xref-"ppi:g435739"
/db_xref-"ppi:g435739"
/translation-"vDLDVSKPDLTTALKEIRAOFEANATSNMQETEEWYRSKFADLT
DASRNTEALRQAKQEANEYRROIOGLTCDLESLRGSNESLERGLREMEERFTIETAG
PASRNTEALEDEIGMLKEEMARHLQEYQDLLNVKLALDIEIATYRKLLEGEESRITVPV
                                                                                                                                                                                                                                                                                                                                                                                                /note-"Description: glial fibrillary acidic protein, Method: conceptual translation with partial peptide sequencing. This sequence comes from Fig. 2" /codon_start-1
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106 A; 42 C; 41 G;
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adult retina
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(GFAP-1) mRNA,
                                                                                                                                                                                                       Score 25; DB 51;
Pred. No. 3.26e-01;
0; Mismatches 10
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Pred. No. 3.26e-01
38; Mismatches 3
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Best Local 9
                                                                                                                      JOURNAL
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1 (bases 1 to 1933)
Glasgow, E. and Schechter, N.
Nucleotide sequence of a GFA
from Goldfish retina
                                                                             Direct Submission
Submitted (07-AUG-1992) G. Wiche, Institute of Biochemistry and Molecular Biology, University of Vienna, Dr. Bohrgasse 9, 1030 Vienna, AUSTRIA
                                                                                                                                                                                             Direct Submission
Submitted (07-AUG-1991) G. Wi
of Vienna, Waehringerstrasse
revised by [3]
                                                                                                                                                                                                                                                                                                                                                              Zauner,W., Kratz,J., Staunton,J., Feick,P.
Identification of two distinct microtubule
recombinant rat MAP 1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRMAP1B5 7095 bp
R.norvegicus mRNA foi
x60370 x60371 x60550
                                                                                                                                                                                                                                                                                 Wiche, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carassius auratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutheria; Rodentia; Sciurognathi; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAP1B gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Cyprininae;
                                                                                                                                                                                                                                                                                                                        92347374
                                                                                                                                                                                                                                                                                                                                                                                                                        Murinae; Rattus.
1 (bases 1 to 7095)
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larity 77.8%;
Conservative
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                                     Location/Qualifiers
1..7095
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LTCDLESLRGSNESLERQLREMEERFATETAGYQDTVARLEDETQMLKEEMARHLOEY
QDLLNVKLALDIETATYRKLLEGEESRITVPVQNFTNLQFRDTSLDTKLTPEAHVKRS
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395 c 507 g 470
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/translation="MGLNDREASYIEKVRFLEQQNKMLVAELNQLRGKEPSRLGDIYQ
EELAELRRQVDGLNAGKARLEIERDNLASDLATLKQRLQEENALRQEAENNLNTFRQD
VDEAALNRVQLERKIDALQDEISFLRKVHEEEMRQLDEQLIAQQVHVDLDVSKRDLTT
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20..1099
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
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1..1933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Carassius
/dev_stage="adult"
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Pred. No. 3.26e-01
0; Mismatches 1
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                                                                                                                                                                                                                      ; G. Wiche,
crasse 17, 1
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binding doma
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Myomorpha;
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/dev_stage="adult"

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Local Similarity 76.1%;
hes 35; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Rutanae; Sapindales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pea.
Pisum sativum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g510542 chalcone synthase; CHS-1A gene; CHS-1B gene; class i gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (01-JUL-1994) R.P. Hellens, John Innes Institute, Colney Lane, Norwich NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to Hellens, R.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hellens, R.P.
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                                                                                                                                                                                                                                                                   /product="naringenin-chalcone synthase"
/db_xref="pi1:9510543"
/db_xref="pi1:9510543"
/translation="myrusiroAqrabgpatyraigtatpqNcveqStypdfyfrit
NSQHKTELKEKFQRMCDKSMIKKRYMHLTEEILKENPSLCEYMAPSLDARQDMVVVEV
PKLGKERATKAIKEWGQPKSKITHLIFCTTSGYDMFADYQLTKLGLRFYVKRYMMY
QOGCFAGGTVLHLAKDLAENNKGARVLVVCSEITAVTFRGPSDTHLDSLYGQALFGDG
AAAVIVGSDPLDVEKPLFELVWTAQTIVPDSEGAIDGHLREAGLTFHLLKDVPSLVS
KNIEKALVEAFQPLNISDYNSIFWIAHPGGPAILDQVEAKLGLKQRKMQATRHVLSEY
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/cell_type="C6 glioma"
1856 c 1799 g 1
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                                                                                                                                                                                  1328..>2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(1040..1217,1328..2319)
/gene="CHS-1A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="linkage group 3"
<1040..1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Pisum sativum"
/strain="JI 813"
/clone_lib="labda GEM-11"
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/product="naringenin-chalcone synthase"
/db_xref="PID:g510544"
                                   'codon_start-1
                                                                       join(4336..4513,4642..5633)
'gene="CHS-1B"
                                                                                                         join(<4336..4513,4642..>5633)
/gene="CHS-1B"
                                                                                                                                               'number='
                                                                                                                                                                'gene="CHS-1A"
                                                                                                                                                                                                 'number-
                                                                                                                                                                                                                /gene="CHS-1A"
                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                       /EC_number="2.3.1.74"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(<1040..1217,1328..>2319)
/gene="CHS-1A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'number=
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                                                        'EC_number="2.3.1.74"
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r chalcone
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Pred. No. 1.38e+00;
0; Mismatches 11
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JOURNAL
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                                                                                                              Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of clone C29F3. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small evertar because we are small evertar because we arrange for a small evertar because we are small e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., Rifken, J., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry, Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryotes; Metazoa; Nematoda;
Eukaryotes; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (21-OCT-1996) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
2. (bases 1 to 18632)
overlap between neighbouring submissions. Coding sequences below are predicted from the program Genefinder (P. Green, ms in p
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368 (6466), 32-38 (1994)
94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matthews, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans
281043
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Similarity 81.6%;
31; Conservative
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PKLGKEAATKALKEWGOPKSKITHLIFCTTSGYDMPGADYQLTKLLGLRCHVKRYMMY
OOGCTAGGTVLRLAKDLAENNKGARTULVYCSELTAVTERGPSDTHLDSLTKOQALFGOR
AAAVIVGSDPLPQVEKPLFELVWTAQTILPDSEGAIDGHLREVGLTFHLLKDVPGLIS
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1307 c
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GNMSSACVLFILDEMRRKSKEEQLGTTGEGLEWGVLFGFGPGLTVETVVLHSVAT"
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to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18632 bp
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Pred. No. 1.38e+00;
0; Mismatches 7
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from computer analysis, using
in preparation), and other
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                           TWNITSSNNKSAPVQAVDQMQNVEQVFSTKSESFYFVSNGGNIKLSTGNRKVQFGFSI
FWDTYQFIQTKUNFSKSATLPPLYSNMPDQOVVITADTRISATIVPPCVKDSFQYLR
GVLFFDGTTRNSTYLGTGLQLLTGKSQYVSTSNQMLISYIGDSMAVNNSPIVLQDVEN
TKSICKFEMILCPDDQDCDGIVSLDGKSQYALQLYHNKFETSFVLNKTLGFGKLEVF
DGGVTKTNLITTYDVNRSELNLPQEFFGRLTTLVFTGETASLTFTRNDDAFDETTSFG
RKGFISSDSYGNSFQEAFHINAPVKNPDTIFKVNIATADLSGSTTLIVYCYRYIELTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(7079..7249,7299..7387,7433..7601,
8197..8292))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="pid:e299497"
/db_xref="pid:e299497"
/db_xref="pid:g1813904"
/translation="MYTIIIFAFFCMFSVEGCIPMTPPEEPVVVPVPVPVPAGWFSFQ
/translation="MYTIIIFAFFCMFSVEGCIPMTPPEEPVVVPVPVPVPAGWFSFQ
RATGLWCYILKPPAAGWTSPQQYCQDNQMGSFVNGFESAAERTQFLQDALAANLAPS
QFLHIGAIRSCAAPPCATTDFYVWQNGVSNDNNFANDYIQLYDGSGQCLSMDLAKNGE
YNDITCDALTAYSCGKYAA"
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HGKETTYSPVKYWLHRDPEQEAEFVEFLLENGESFTLTEKHLVFATDCQQNVKNLDDL
NPTSTGKINIGECFFMAQPEVRSSLYCV"
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/db_xref="pID:e399269"
/db_xref="pID:91813905"
/db_xref="pID:91813905"
/t-ans1ation="MrpadnryvsnalaaetfvpgeHsrrrrweftsnlovglarprd
KKILSFRRHCHRVERWTCGRIANRLFPTIQLLTGSMNYLLLVSGLLSVWQPVFGSRCG
ESTIPFSLEILPSGHPVLGCARPTCFGWHPKGYQLPTTAKFSKLNRKLDGFLRDDSLF
                                                                                                                                                                                                                  complement(join(15422..15713,16068..16591,16640..17140,
17376..18179))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="Myperstfedhsrdvfleqenvelfgflvavehdvsvlthfiis
lnrfisvmcpifyktmenlkktyklfifavmliseligslehivlcrirenadlileti
ilapsycfelgrygdlefnscivilmildvetlikvklisneikksvsedavogets
rdrrflaqavtqgslellatmvffptrfsvnswvtflggnscgrwinvpqnyfatiql
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RESTDRNIATVSAGEIVIGGEVYQNESQYAFDYISNIEKSMDEMGEVYYEVNIRKFAC
LDPHHADARKLDEVWSSENTIKKVNGGKPIAQQAPNYAVNAPIEAGTFDGEVUDGGTV
IEEIIAQQGFIVENETTVAPFAGPFQAQGFQPRFGAPQGFQPAFQQPPPQQFFPQNFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(158..341,421..598,647..698,743..796,845..1128,1176..1414,1456..1544,1591..1788,2036..2301
                                                                                                                                                                                                                                                                                                                          ELSFNSTNLPPLNTTITFHGNFLHIEYYPNGTDSSKLFLNFDIEKSVTRSSEFFFACV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="C29F3.e"
/db_xref="PID:e299270"
/db_xref="PID:g1813906"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(10724..10982,11039..11394,12940..13052,13183..13295,
13344..13893,13948..14262,14952..15141)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mhwrltvlffasaqlsegclpmvppeepvtpvpvcpagwfqfqr
ATGLWCYIFATPGAGWTTPQAACQANYGANLNGFESAAERTQFIQDMLASNLAPYTFV
/product="C29F3.a"
/db_xref="PID:e299496"
                                                                                                                                                                             /note="protein predicted using Genefinder'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note-"protein predicted using Genefinder"
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/db_xref="PID:g1813903"
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SOURCE

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Homo sapiens

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TITLE
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SOURCE
                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
       KEYWORDS
                                                 ACCESSION
                                                                                           DEFINITION
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                                                                                                                                                                                                                                                                                               Query Match 1.6%;
Best Local Similarity 90.0%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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Caenorhabditis elegans.

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;

Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabdito

Rhabditidae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (04-NOV-1996) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Order of segments is not known; 800 n's separate segments.
g1780984
HTG; HTGS_PHASE1.
                                                                      Human DNA sequence
799F10; HTGS phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Order of segments is not known; 800 n's separate segments. Cosmid=T09D4; Contig ID=00659; Length=42147; Status=Unfinished Cosmid=T09D4; Contig ID=01673; Length=1019; Status=Unfinished Cosmid=T09D4; Contig ID=01596; Length=1665; Status=Unfinished Cosmid=T09D4; Contig ID=01600; Length=1271; Status=Unfinished.
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KFVLDAVILKAKNKLIKLIYONUP APLKILDVVRTAYLDRKÜĞYEABAKARĞELSQI
FQSKALFGLFEGSTNAKKNKYĞKĞLPVNEIAVVĞAĞFMĞAĞIANVTINKĞIRTIYLLDA
NQAĞVERĞONIYATHLMRQLKAÇKISKLEREKIYNLƏVIDYSAMKNADVVLEAVFE
DLEKKHKVIĞLENVÇĞNTIIASMIŞALPIKDIAAKSSISKVIĞMIŞFŞVYEKNOL
LEIITHDĞTSKETLATAAQLĞLKQĞKLVVVVKDÇPĞFFVVRÇLSPMMSEIVRLLOĞĞV
EPSELDKITIKEĞF PYĞAATLADEĞĞLDVAKIYARYLĞTALĞFYHĞĞĞYDLLİSELVR
NGHKÇRKTSKÖIFVYĞDĞAKĞSKYNQEAKLFEKYKLTALĞAÇVĞĞÇYDLLİSELVR
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Pred. No. 1.3
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                                                                                           SEQUENCING IN PROGRESS ***
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                                                                                                                                            g165225
formaldehyde dehydrogenase; ABC transporter; DNA ligase; DNA
polymerase III alpha subunit; GumB protein; LysR transcriptional
regulator; Mg.protoporhyrin IX; N-acetylornithine aminotransferase;
NADH dehydrogenase subunit 4; NADH dehydrogenase subunit 5; acetate
kinase; aspartoacylase(ASP); cation-transporting ATPase; cell
division protein FtsH; chemotaxis protein Chap; cytochrome oxidase
d subunit I; cytochrome oxidase d subunit II; dienelactone
hydrolase; dihydroflavonol 4 reductase; dihydropterate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hunt,
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 115419)
pyrophosphorylase; esterase; ferrous iron transport protein B; fibrillin; formaldehyde dehydrogenase (glutathione); high light-inducible protein; leader peptidase I; lysostaphin; malonyl coenzyme A-acyl carrier protein transacylase; methyl-accepting chemotaxis protein (MCP); oligopeptide transport ATP-binding
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a single finished sequence with
Location/Qualifiers
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larity 80.0%;
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/clone="799F10"
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Contig_ID: 00949

Contig_ID: 00968

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630555-781448.
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MEDLINE
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TITLE
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Submitted (28-JUN-1996) to the DDBJ/EMBL/GenBank databases. Satoshi Tabata, Kazusa DNA Research Institite, Laboratory of Gene Structure 2; 1523-3; Yanauchino, Kisarazu, Chiba 292; Japan (E-mail:tabata@kazusa.or.jp, Tel:+81-438-52-3933, Fax:+81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miyajima, N., Hirosawa, M., Sugiura, M., Sasamoto, S., Kimura, T., Hosouchi, T., Matsuno, A., Muraki, A., Nakazaki, N., Naruo, K., Okumura, S., Shimpo, S., Takeuchi, C., Wada, T., Watanabe, A., Yasuda, M. and Tabata, S. Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions and assignment of potential protein-coding regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthetase; sporulation protein SpoIID; sulfolipid biosynthesis protein SqdB; tRNA-Arg; tRNA-Leu; tyrosyl tRNA synthetase. Synechocystis sp. (strain: PCC6803) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein OppF; oxygen independent coprophorphyrinogen III oxidase; penicillin-binding protein 1B; phenoxybenzoate dioxygenase; phycocyanin a subunit; phycocyanin associated linker protein; phycocyanin b subunit; potassium channel; protein conferring resistance to acetazolamide, Zam; regulatory component of sensory transduction system; regulatory components of sensory transduction system; ribonuclease II; sensory transduction histidine kinase; system; ribonuclease II; sensory transduction histidine kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (Sites)

Kaneko,T., Sato,S., Kotani,H., Tanaka,A., Asamizu,E., Nakamura,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bubacteria; Cyanobacteria; Chroococcales; Synechocystis.
1 (bases 1 to 150894)
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EKQLSVPLEDBGGRKAQLTEAGHLLLNYGEKIITLCGTCRAEDLQNLQGGTLIVGA
SQTTGTYLLPARIGHERQCYEPOTVOLQVHSTRRTARGVANGQVDLAIIGGEVPAELO
ETLTVLPYAEDELALILPVLHPLAQAETIQKEDLYKLKFISLDSQSTIRKVIDKVLSQ
                                                                                                             /translation="MENSPYRPMRYGFYTLDYFTDQLFGGNPLAYFPDAEGLTDGQMQ KIAAEINYSETYFYLFPYTETGNFRLALFTPKRELDFAGHFTGTTYLLGLLQFPSPL YTTTWQLEEPYGLYFYLHYKQGGLYGTELTAKQLPGTKDSAPSCEDLALLLGLSDD QQGSYEPQAXSCGLDFLFIPLINEEALNRISFNPSYWQNLLAGQWADCYYCLAPGDP SLGLSDNKLIHGRMFAPGLGIAEDPATGSGVAALGGYLDDRLDTPGSHHWQIEQGKAL
                                                                   GRPSQLQLTVVKDGQGIRAVKVAGRSVLVSEGFMNLGN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1342..1539)
/note="ORF_ID:ss11911"
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/note="ORF_ID:s110998"
                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein"
/db_xref="PID:g1652228"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQGKPQSSFRTTYDRSNASLS"
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/db_xref="PID:g1652227"
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/db_xref="PID:g1652226"
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'product="tRNA-Leu"
                                                                                                                                                                                                                                                                                                                       transl_table=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MSTQQQARALMMRHHQFIKNRQQSMLSRAAAEIGVEAEKDFWTT"
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ETLTP!AP!RQRLDRWYELTGKKIDLF!GDINDYPF!INALRQFQPDAVVHGEQQRSA 
PFSMIDREHAVLTQANNVLGNLNLYALKEDFPDCHLYKLMGEYGTPNLD!EEGY! 
TIEHKGRKDTLPYPKQPGSFYHLSKYHDSHN!HFACK!WGLRATDLNQG!VYGVLTEE 
TGMDEMLINRLDYDGVFGTALNRFC!QAA!GHDLTVYGKGGQTRGLLD!RDTVBC!EL 
AIANPADKGQFRYFNQYTELFSYGDLAQMYQKAGADLGLKVEIDHLENPRVELEEHYF
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LGIICCLGLMIISGDGDEDLDVBMSLEASSDVDITHLDVELDGGEDMEEGEAVPMALQV
LSFFGLGKVPLMILLGIDFSLWGVCIGWILNVTVATVTGTMPRELMGWAGIIFLVVSLA
LSFFGLGKVPLMILLGIDFSLWGVCIGWILDVTTVSKKLPYLANGTIGQAHVYDNAG
                                                                                                                                                                                                                                                                                                                                                                                    /translation="MTVALDREIIYPDSDGQPMADNTEQFEWIVLLKENLECLFAHNP
DVFVGGDLLWYPVEGHPEIRVAPDVMVALGRPKGKRGSYRQWQENNQAPQVVFEILSP
GNTLKEMTKKLKFYDHHGVEEYYVYDPDDNELTGLQRIGGELTIIEEMAHWVSPLLGI
NLITISVSLPDWATVIPHHNQEILIIDQSPKGYGYLAIAKDSSDEDKWLKS"
complement(8962..10059)
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Plsacalipsppavegnqqvingrpepyolosdyyfpipdisdepkingkvekg
DVsasIsyroskhdoyesmppyvvkeknkivaliegsespkijalojpepkingknpyp
PAVLFATYTGGAHCCNEYKYFISNQNGSDMSVRDFGFFNGGPHPAEDLNNDGWDEYVE
                                                                                                                                                                                                                                                                                                     complement(8220..9029)
                                                                                                                                                                                                                                                                                                                                    RLKALLAEAGIDV"
                                                                                                                                                                                                                                                                                                                                                           KFELSAETLRVYYPDGRPFLSTVALATQAEQASQRANEEAQRAEREKLRAELAEAEND
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/db_xref="PID:g1652233"
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/note="ORF_ID:s110996"
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QDSEKNGFLAAYVANKALIGELDEGWQTMLKYYDRESDWGLTNCLEYDDQSNCLNEVK
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/note="ORF_ID:s110997"
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/db_xref="PID:g1652232"
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/db_xref="PID:g1652231"
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/db_xref="PID:g1652230"
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                                                                                                                                                                                        'product="hypothetical protein"
'db_xref="PID:g1652234"
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Matches
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Note: remainder of annotations omitted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E. coli aceA gene coding X07543
                                                                                                                                                                                                                                                 Submitted (06-MAY-1988) Cozzone A.J., University of Lyon, Laboratory of Molecular Biology, 43 Boulevard du onze Novembre,
                                                                                                                                                                    69622 Villeurbanne, France 2 (bases 1 to 1344) Rieul, C., Bleicher, F., Duc.
                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
                                                                                                         Escherichia coli
                                                                                                                                       Nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                               Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 1.6%;
Similarity 81.6%;
31; Conservative
                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 1344)
                                                                                     eic Acids
Location/Qualifiers
1..1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGRTLATITÄTGQFKYQQYFDPLVPGFDYVPYNDIRSLENKYADLDEGNSRVAAIFLE
PLQGEGGVRPGDLAYKKRVDEDLOQNDILLVPDEVQVGVGRTGKLWGYEHLGVEDIF
TSAKGLAGGVPIGAMMCKKFCDVFBCNHASTFGGNPLACAAGLAVLKTIEGDRLLDN
VQARGEQLRSGLAEIKNQYFTLFTEVRGWGLINGLEISAESSLTSVEIVKAAMEDGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYVEDWTWLDAFYMTTITLATVGFGETHPLSPASRLFTILLILMGLLTIGYMVNRFTE
AFIQGYFQDSLRRRQEOKVIERLADHYILCGYGRTGQQIAFEFAVENIPFVVIDASPE
VIIQAKLRDYAVLQGDATLDEILLAAHIERAICIVSALSSDAENLYTVLSAKTLNPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIARGQGSTLMDTEGKSYLDFVAGIATCTLGHAHPALVRAVSDQIQKLHHVSNLYYIP
EQGELAKWIVEHSCADRVFFCNSGAEANEAAIKLVRKYAHTVLDFLEQPVILTAKASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAIARASSEEAVQKLKRAGADEVVSPYITGGKRLAAAALRPQVVSFVDGILTGADRSF
YMEEFRIGAEDCPYIGQTLREAQLRAQSGALILAIRRQDRKLIVGPMGDTHLLDADSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein"
/db_xref="PID:g1652237"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAPAGPKVLRFVPPLVVTEAEIAQAVEILRQAIATLV'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="potassium channel"
/db_xref="PID:g1652235"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .1920..12561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="ORF_ID:slr1023"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MTYSPVVESVEAQAFAVTDLSPAAEFKTADFDTYVMNTYGRFPI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="N-acetylornithine aminotransferase"
/db_xref="PID:g1652236"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="ORF_ID:slr1022"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="argD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICLGTVEQLRALNQLLCPLNPARVRLPKNHR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="ORF_ID:s110993"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isocitrate lyase; isocitritase
                                                                                  16 (12), 5689 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24; DB 20; Le
Pred. No. 1.38e+00;
0; Mismatches 7;
                                                                                                                                          Duclos, B., Cortay, J.C. and Cozzone, A.J. the aceA gene coding for isocitrate lyase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for isocitrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 150894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Search completed: Thu Aug 21 10:01:07 1997 Job time : 2597 secs.

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